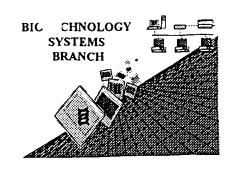
BEST AVAILABLE COPY

RAW SEQUENCE LISTING ERROR REPORT





The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/831, 926Source: 13c + 09Date Processed by STIC: 5-23-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING DATE: 05/23/2001 TIME: 15:44:24 PATENT APPLICATION: US/09/831,426 **Does Not Comply** Corrected Diskette Needed Input Set : A:\2503.APP.txt global errors Output Set: C:\CRF3\05232001\I831426.raw 3 <110> APPLICANT: Hoechst Marion Roussel 5 <120> TITLE OF INVENTION: HUMAN htFIII GENE AND CODED htfIIIA PROTEIN 7 <130> FILE REFERENCE: 9823seq C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/831,426 C--> 10 <141> CURRENT FILING DATE: 2001-05-08 12 <160> NUMBER OF SEQ ID NOS: 10 14 <170> SOFTWARE: PatentIn Vers. 2.0 ERRORED SEQUENCES -> Valid responses: DNA, BNA, PBT. 16 <210> SEQ ID NO: 1 17 <211> LENGTH: 1273 E--> 18 <212> TYPE: ADN -19 <213> ORGANISM: Human 21 <220> FEATURE: Correct:

<400> 1 26 atgcgcagca gcggcgccga cgcggggggg tgcctggtga ccgcgcgcgc tcccggaagt 60 Bespond with 28 gtgccggcgt cgcgcgaagg ttcagcaggg agccgtgggc cgggcgcgcc ggttcccggc 120 30 acgtgtctcg gcacgtggca gcgcgcctgg ccctgggctt ggaggcgccg gcgcc ctg 31 no text.

32 34 gat eeg eeg gee gtg gte gee gag teg gtg teg tee ttg ace ate gee 35 Asp Pro Pro Ala Val Val Ala Glu Ser Val Ser Ser Leu Thr Ile Ala 38 gac gcg ttc att gca gcc ggc gag agc tca gct ccg acc ccg ccg cgc 274 39 Asp Ala Phe Ile Ala Ala Gly Glu Ser Ser Ala Pro Thr Pro Pro Arg 42 ccc gcg ctt ccc agg agg ttc atc tgc tcc ttc cct gac tgc agc gcc 322 43 Pro Ala Leu Pro Arg Arg Phe Ile Cys Ser Phe Pro Asp Cys Ser Ala 40 370 46 aat tac age aaa gee tgg aag ett gae geg eac etg tge aag eac aeg 47 Asn Tyr Ser Lys Ala Trp Lys Leu Asp Ala His Leu Cys Lys His Thr 60 55 50 ggg gag aga cca ttt gtt tgt gac tat gaa ggg tgt ggc aag gcc ttc 418 51 Gly Glu Arg Pro Phe Val Cys Asp Tyr Glu Gly Cys Gly Lys Ala Phe

466 54 atc agg gac tac cat ctg agc cgc cac att ctg act cac aca gga gaa 55 Ile Arg Asp Tyr His Leu Ser Arg His Ile Leu Thr His Thr Gly Glu 58 aag ccg ttt gtt tgt gca gcc act ggc tgt gat caa aaa ttc aac aca 514 59 Lys Pro Phe Val Cys Ala Ala Thr Gly Cys Asp Gln Lys Phe Asn Thr 110 105 62 aaa tca aac ttg aag aaa cat ttt gaa cgc aaa cat gaa aat caa caa 562 63 Lys Ser Asn Leu Lys Lys His Phe Glu Arg Lys His Glu Asn Gln Gln

The types of errors shown exist throughout the Sequence Listing. Please check file://C:\Crf3\1 subsequent sequences for similar errors.

Input Set : A:\2503.APP.txt

Output Set: C:\CRF3\05232001\1831426.raw

64		115					120					125					
-	222		tat	ata	tac	ant		maa	a a c	tat	aan	-	acc	+++	aan	222	610
													Thr				010
	130	GIII	ıyı	TIE	Cys	135	FIIC	GIU	тэћ	Суз	140	_	1111	1116	шуз	145	
		~~~	000	ata	222		ant	a 2 a	+ ~~	~~~			aat	<b>~</b> ~ ~	aat		658
																	030
	HIS	GIN	GIN	Leu	_	тте	птѕ	GTII	Cys	155	птэ	1111	Asn	GIU	160	Leu	
72	4-4		4 4-		150									<b>.</b>			706
													gca				706
	Phe	Lys	Cys		Gin	GIU	GIA	Cys		ьуѕ	HIS	Pne	Ala		Pro	ser	
76				165					170					175			254
													gta				754
	Lys	Leu	-	Arg	Hls	Ala	ьys		His	GIU	GLY	Tyr	Val	Cys	GIN	гàг	
80			180					185					190				
													ctg				802
83	Gly	-	Ser	Phe	Val	Ala	_	Thr	Trp	Thr	Glu		Leu	Lys	His	Val	
84		195					200					205	•				
													tgc				850
87	Arg	Glu	Thr	His	Lys	Glu	Glu	Ile	Leu	Cys		Val	Cys	Arg	Lys		
88	210					215					220					225	
90	ttt	aaa	cgc	aaa	gat	tac	ctt	aag	caa	cac	atg	aaa	act	cat	gcc	cca	898
91	Phe	Lys	Arg	Lys	Asp	Tyr	Leu	Lys	Gln	His	Met	Lys	Thr	His	Ala	Pro	
92					230					235					240		
													gga				946
95	Glu	Arg	Asp	Val	Cys	Arg	Cys	Pro	Arg	Glu	Gly	Cys	Gly	Arg	Thr	Tyr	
96				245					250					255			
98	act	act	gtg	ttt	aat	ctc	caa	agc	cat	atc	ctc	tcc	ttc	cat	gag	gaa	994
99	Thr	Thr	Val	Phe	Asn	Leu	Gln	Ser	His	Ile	Leu	Ser	Phe	His	Glu	Glu	
10	0		260	)				265	5				270	)			
10	2 ago	c cgc	c act	: ttt	gto	g tgt	gaa	a cat	gct	gge	tgt:	t gg	c aaa	a aca	a ttt	gca	1042
																e Ala	
10	4	27	5			_	280	)				28	5				
10	6 ato	aaa	a caa	agt	cto	act	ago	g cat	: gct	gtt:	gta	a cat	t gat	cct	gad	aag	1090
																Lys	
	8 290	-				295	_	-			300		_			305	
11	o aad	a aaa	a ato	aac	cto	aaa	qto	aaa	a aaa	a .t.ct	cgt	t gaa	a aaa	a cgg	g agt	ttg	1138
																Leu	
11		_		-	310			_	_	315			_		320		
		e tet	t cat	cto	agt	. qqa	a tat	ato	c act	ccc	c aaa	a aq	g aaa	a caa	a ggo	g caa	1186
																Gln	
11				325		_	•		330		-			335	-	•	
		tta	a tot			. caa	aaa	c aaa	a gad	ı tca	a cc	c aa	e tat	gto	g qaa	a gac	1234
11	9 G1	z Lei	ı Sei	r Lei	1 Cvs	Glr	Asr	1 G1	/ Gli	ı Sei	c Pro	o Ası	n Cvs	s Val	ĺĞlι	ı Āsp	
12		, 20.	340				• • • • •	345					350				
		r ato			r aca	a att	g a ca			aco	c cti	t aa	c taa				1273
	3 Lys																
12	_	35					360				,	36					
				א מו	): 2			-									
	127 <210> SEQ ID NO: 2 128 <211> LENGTH: 365																
	9 <2:																
					_												

Input Set : A:\2503.APP.txt

Output Set: C:\CRF3\05232001\I831426.raw

E>	130	<213	3> OF	RGAN	ISM:	Huma	an	_	>	< c 0	.ھ <	1					
E>	132	<400	)> SE	EQUE!	Pro	0 -	Val	Val	Δ1=	Glu	Ser	Val	Sor	Ser	Len	Thr	Tle
	134	1	нар	FIO	FIO	5	vaı	vai	nia	Giu	10	VQI	Der	Der	Leu	15	116
		_	Asp	Ala	Phe 20	Ile	Ala	Ala	Gly	Glu 25	Ser	Ser	Ala	Pro	Thr 30	Pro	Pro
		Arg	Pro	Ala 35	Leu	Pro	Arg	Arg	Phe 40		Cys	Ser	Phe	Pro		Cys	Ser
		Ala	Asn 50		Ser	Lys	Ala	Trp 55	_	Leu	Asp	Ala	His 60		Cys	Lys	His
		Thr 65		Glu	Arg	Pro	Phe 70		Cys	Asp	Tyr	Glu 75	Gly	Cys	Gly	Lys	Ala 80
			Ile	Arg	Asp	Tyr 85	His	Leu	Ser	Arg	His 90	Ile	Leu	Thr	His	Thr 95	Gly
		Glu	Lys	Pro	Phe 100	Val	Cys	Ala	Ala	Thr 105	Gly	Cys	Asp	Gln	Lys 110	Phe	Asn
		Thr	Lys	Ser 115	Asn	Leu	Lys	Lys	His 120	Phe	Glu	Arg	Lys	His 125	Glu	Asn	Gln
	157 158	Gln	Lys 130	Gln	Tyr	Ile	Суѕ	Ser 135	Phe	Glu	Asp	Суѕ	Lys 140	Lys	Thr	Phe	Lys
		Lys 145	His	Gln	Gln	Leu	Lys 150	Ile	His	Gln	Cys	Gln 155	His	Thr	Asn	Glu	Pro 160
	164			-	Cys	165			_	-	170					175	
	167		_		Lys 180					185					190		
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	173		210		Thr			215					220				
	176	225		-	Arg	-	230	_		_		235					240
	179			_	Asp	245					250					255	
	182	-			Val 260					265					270		
	185			275	Pro				280					285			
	188		290	_	Gln			295					300				
	191	305			Met		310					315					320
	194				His	325					330		·			335	
	197		_		Ser 340					345					Cys 350	Val	GIu
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Input Set : A:\2503.APP.txt

Output Set: C:\CRF3\05232001\I831426.raw

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     213 acgtgtctcg gcacgtggca gcgcgcctgg ccctgggctt ggaggcgccg gcgccctgga 180
     215 tecgeeggee gtggtegeeg agteggtgte gteettgace ategeegaeg egtteattge 240
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     243 tggctgtggc aaaacatttg caatgaaaca aagtctcact aggcatgctg ttgtacatga 1080
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Input Set : A:\2503.APP.txt

Output Set: C:\CRF3\05232001\I831426.raw

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VERIFICATION SUMMARYDATE: 05/23/2001PATENT APPLICATION: US/09/831,426TIME: 15:44:25

Input Set : A:\2503.APP.txt

Output Set: C:\CRF3\05232001\I831426.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:18 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:25 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0 L:132 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0 L:205 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:208 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0 L:256 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:259 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0 L:305 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:308 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0 L:314 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:317 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:0 L:323 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:0 L:332 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:335 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:0 L:341 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:344 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:0 L:350 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: L:353 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:0